

BLAST Basic Local Alignment Search Tool

Appendix C

[Edit](#) and [Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

Protein Sequence (223 letters)

Results for: [lcl|54117](#) [None\(223aa\)](#)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

[lcl|54117](#)

Description

[None](#)

Molecule type

[amino acid](#)

Query Length

[223](#)

Subject ID

[gil6706916|gb|AAF25499.1|AF058942_3](#)

Description

[spike glycoprotein \[bovine coronavirus\]](#)

Molecule type

[amino acid](#)

Subject Length

[1363](#)

Program

[BLASTP 2.2.22+](#) [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

[Reference - compositional score matrix adjustment](#)

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#)

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hittist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

Karlin-Altschul statistics

[Params](#) [Ungapped](#) [Gapped](#)

Lambda	0.323458	0.267
K	0.140461	0.041
H	0.463759	0.14

Results Statistics

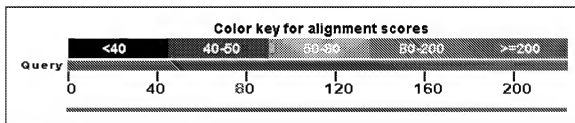
Effective search space 249664

Graphic Summary

Distribution of 5 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Plot of lcl|54117 vs gi|6706916|gb|AAF25499.1|AF058942_3 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Sequences producing significant alignments:	Score (Bits)	E Value
gb AAF25499.1 AF058942_3 spike glycoprotein [bovine coronavirus]	436	7e-127

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>gb|AAF25499.1|AF058942_3 spike glycoprotein [bovine coronavirus]
Length=1363

Score = 436 bits (1122), Expect = 7e-127, Method: Compositional matrix adjust.
Identities = 220/223 (98%), Positives = 221/223 (99%), Gaps = 0/223 (0%)

Query 1	NHIIISLVQNPAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNNTWMT	60
Sbjct 1141	NHIIISLVQNPAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNNTWMT	1200
Query 61	GSYYYYPEPIITGNVVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTLMAPD	120
Sbjct 1201	GSYYYYPEPIITGNVVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTLMAPD	1260
Query 121	LSLDYINVTFDLQDEMNRRLQEAIKVLNHSYINLKDIGTYEYVWKWPYVWLLIGLAGVA	180
Sbjct 1261	LSLDYINVTFDLQDEMNRRLQEAIKVLNHSYINLKDIGTYEYVWKWPYVWLLIGLAGVA	1320
Query 181	MLVLLFFICCTGCGTSCFKKCGGCCDDYTGHQELVIKTSDD	223
Sbjct 1321	MLVLLFFICCTGCGTSCFKKCGGCCDDYTGHQELVIKTSDD	1363

Score = 23.1 bits (48), Expect = 0.025, Method: Compositional matrix adjust.
Identities = 16/62 (25%), Positives = 29/62 (46%), Gaps = 5/62 (8%)

Query 85	YTKAPDVMLNISTPNLPDFKEELDQWFKNQTLMAPDLSLDYINVTFDLQDEMNRRLQEA	144
Sbjct 313	YTVQPIADVYRRIPNLPDCN--IEAWLNKDSVPSP---LNWERKTFNSCNFNMSLSFI	367
Query 145	KV 146	
Sbjct 368	QA 369	

Score = 20.8 bits (42), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 9/30 (30%), Positives = 13/30 (43%), Gaps = 0/30 (0%)

Query 14	LYFIHFSYVPTKYVTAKVSPGLCIAGDRGI	43
Sbjct 474	VYAQCFCFAPNTFCPCCKLDGSLCVSGSGI	503

Score = 17.7 bits (34), Expect = 1.2, Method: Compositional matrix adjust.
Identities = 9/24 (37%), Positives = 12/24 (50%), Gaps = 0/24 (0%)

Query 34	GLCIAGDRGIAPKSGYFVNNTIW	57
Sbjct 629	GVCVNYDLGITGQGFVEVNTAT	652

Score = 17.3 bits (33), Expect = 1.4, Method: Compositional matrix adjust.
 Identities = 7/24 (29%), Positives = 14/24 (58%), Gaps = 0/24 (0%)

```
Query   55   NTWMFTGSGYYYPEPITGNNVVVM   78
          N ++ T  +YY P+T N+ + +
Sbjct  235   NVYLGIVLSHYVVMPLTCNSAMTL 258
```

Select All Get selected sequences Distance tree of results Multiple alignment **NEW**